



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/538,038A

DATE: 06/20/2006
TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT
Output Set: N:\CRF4\06202006\J538038A.raw

2 <110> APPLICANT: Givaudan SA
W--> 3 <120> TITLE OF INVENTION: G-Proteins
W--> 4 <130> FILE REFERENCE: 30069PCT
W--> 5 <140> CURRENT APPLICATION NUMBER: US 10/538,038A
C--> 6 <141> CURRENT FILING DATE: 2005-06-08
7 <150> PRIOR APPLICATION NUMBER: US 60/434,790
8 <151> PRIOR FILING DATE: 2002-12-18
W--> 9 <160> NUMBER OF SEQ ID: 2

ERRORED SEQUENCES

W--> 10 <210> SEQ ID NO: 1
11 <211> LENGTH: 1122 <212> DNA
12 <213> ORGANISM: Homo sapiens
W--> 13 <220> FEATURE:
14 <221> NAME/KEY: CDS
15 <222> LOCATION: (1)..(1122)
16 <223> OTHER INFORMATION:

~~E--> 17 <212> TYPE: ignore this~~

W--> 17 <400> SEQUENCE: 1

18 atggcccgcct cgetgacctg gcgctgctgc ccctgggtgcc tgacggagga tgagaaggcc 60
19 gccgcccggg tggaccagga gatcaacagg atcctcttgg agcagaagaa gcaggaccgc 120
20 ggggagctga agctgctgct tttgggcccc ggcgagagcg ggaagagcac cttcatcaag 180
21 cagatgcgga tcatccacgg cgccggctac tcggaggagg agcgcaaggg cttccggccc 240
22 ctggtctacc agaacatctt cgtgtccatg cgggccatga tcgaggccat ggagcggctg 300
23 cagattccat tcagcaggcc cgagagcaag caccacgcta gcctgggtcat gagccaggac 360
24 ccctataaag tgaccacgtt tgagaagcgc tacgtgcgg ccatgcagtg gctgtggagg 420
25 gatgccggca tccgggacct ctatgagcgt cggcggggaat tccacctgct cgattcagcc 480
26 gtgtactacc tgtcccacct ggagcgcctc accgaggagg gctacgtccc cacagctcag 540
27 gacgtgctcc gcagcgcgat gccaccact ggcacaaag agtactgctt ctccgtgcag 600
28 aaaaccaacc tgcggatcgt ggacgtcggg ggccagaagt cagagcgtaa gaaatggatc 660
29 cattgtttcg agaacgtgat cgccctcatc tacctggcct cactgagtga atacgaccag 720
30 tgcctggagg agaacaacca ggagaaccgc atgaaggaga gcctcgcat gtttgggact 780
31 atcctggaac taccctggtt caaaagcaca tccgtcatcc tctttctcaa caaaaccgac 840
32 atcctggagg agaaaatccc caccctccac ctggctacct atttccccag tttccagggc 900
33 cctaagcagg atgctgaggc agccaagagg ttcacacctg acatgtacac gaggatgtac 960
34 accgggtgcg tggacggccc cgagggcagc aacttaaaaa aagaagataa ggaaatctat 1020
35 tctcacatga cctgcgctac tgacacacaa aacgtcaaat tcgtgtttga tgccgtgaca 1080
36 gatataataa taaaagagaa cctcaagac tgtgggctct tc 1122

38 <210> SEQ ID NO: 2
39 <211> LENGTH: 374
40 <212> TYPE: PRT

? (see p.3 - the last-numbered amino acid states "390")

Does Not Comply
Corrected Diskette Needed

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41 <213> ORGANISM: Homo sapiens
W--> 42 <400> SEQUENCE: 2
43 Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
E--> 44 5 10 15 10 15
46 Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
E--> 47 20 20 25 30
49 Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu
E--> 50 35 40 45
52 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
E--> 53 50 55 60
55 Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
E--> 56 65 70 75 80
58 Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
E--> 59 85 90 95
61 Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
E--> 62 100 105 110
64 Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
E--> 65 115 120 125
67 Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile
E--> 68 130 135 140
70 Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
E--> 71 145 150 155 160
74 Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val
E--> 75 165 170 175
77 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
E--> 78 180 185 190
80 Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
E--> 81 195 200 205
83 Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
E--> 84 210 215 220
86 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
E--> 87 225 230 235 240
89 Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
E--> 90 245 250 255
92 Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
E--> 93 260 265 270
95 Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
E--> 96 275 280 285
98 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
E--> 99 290 295 300
101 Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
E--> 102 305 310 315 320
104 Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Asn Leu Lys Lys Glu Asp
E--> 105 325 330 335
107 Lys Glu Ile Tyr Ser His Met Thr Cys Ala Thr Asp Thr Gln Asn Val
E--> 108 340 345 350
110 Lys Phe Val Phe Asp Ala Val Thr Asp Ile Ile Ile Lys Glu Asn Leu
E--> 111 355 360 365
113 Lys Asp Cys Gly Leu Phe Ser His Leu Ala Thr Tyr Phe Pro Ser

delete

misaligned

*amino acid
numbers*

*(see item 3
on Error*

Summary

Sheet 1

Invalid amino acid designator

Q17

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E--> 114 370 375 380
E--> 116 Phe Gln Gly Pro Lys Gln Asp
E--> 117 385 390

invalid amino acid designator
Gln

VERIFICATION SUMMARY

DATE: 06/20/2006

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Input Set : A:\Sequence Listing.TXT

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L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:283 W: Missing Blank Line separator, <140> field identifier
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <220> field identifier
L:17 M:282 E: Numeric Field Identifier Missing, <212> is required.
L:17 M:283 W: Missing Blank Line separator, <400> field identifier
L:17 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:16
L:42 M:283 W: Missing Blank Line separator, <400> field identifier
L:44 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:98 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:116 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1